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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                         Database
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                              seq length: 0
seq length: 2000000000
PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 ,
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3532
                                                                                                                                                                                                                                                                      195891 seqs, 67900655 residues
                                                                                                                                                                                                                                                                                                                                                             1 MAINTSNLCSLLFLLSLFLL.....SSRSTKQQQPLVSILDFVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                        Gapext 0.5
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264.889 Million cell updates/sec
                                                                                                                                                                                                                                      195891
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	2 00	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	NO.	Result	
332.3	557	565	568	682.5	689.5	704.5	711.5	715.5	727	748	749.5	760.5	760.5	765	770.5	798	832.5	855.5	859.5	872.5	875	895	902	1022.5	1083.5	1092	1142	1191.5	SCOLE		
T3.6	15.8	16.0	16.1	19.3	19.5	19.9	20.1	20.3	20.6	21.2	21.2	21.5	21.5	21.7	21.8	22.6	23.6	24.2	24.3	24.7	24.8	25.3	25.5	28.9	30.7	30.9	32.3	33.7	Macch Length	Query	æ
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SOUTSU	A24810	S10156	A23498	S00281	JQ2264	FWPMVB	S06309	A27288	S15675	FWSYCB	S35757	S08505	S00567	S24756	T06459	JQ1730	S00566	FWSYBA	S20007	B24810	S35221	B53234	A53234	S08059	FWCNAB	S06398	S22477	T44430	10	1	
vicilin - Zamia iu	phaseolin beta cha	alpha-phaseolin pr	phaseolin type alp	canavalin - sword	canavalin - jack b	vicilin B precurso	vicilin precursor	vicilin precursor	globulin-2 precurs	beta-conglycinin b	vicilin, 47K - gar	vicilin - garden p	vicilin precursor	vicilin-like stora	62K sucrose-bindin	62K sucrose-bindin		beta-conglycinin a	beta-conglycinin a	beta-conglycinin a	globulin Begl prec	vicilin-like stora	globulin-18, GLBIS	alpha-globulin typ	alpha-globulin B p	alpha-globulin typ	vicilin precursor	protein PV100 [imp	Description		
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ERFSERSELLKGIKNORLALLEARPHTFIVPHHLDAECVLLVVRGRATITTVVQEKRETR 472

ALIGNMENTS

protein PV100 [imported] - winter squash (C;Species: Cucurbita maxima (winter squash) C;Cspecies: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T44430 #sequence_revision M: Nishimura, M: Hara-Nishimura, I.

Biol. Chem. 274, 2563-2570, 1999
A;Fitle: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin A;Reference number: Z22767; MUID:99107919
A;Reference number: T44430
A;Recession: T44430
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <YAMD
A;Residues: 1-810 <YAMD
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062 δõ B Qy DЬ DЬ Qy ф Ş Ъ Š DЬ Q Вр Query Match Best Local Similarity Matches 284; Conserv 274 ENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNR----353 293 154 179 121 233 RRGGRDDEDENQRDPDWRREQKRREQEQERRERERRGGRDDEDENQRDPDWRREQERREQ 94 66 61 32 ------DRQEYEECKRQCMQLETS-GQMRRCVSQCDKRFEE------۳ SGPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERR 153 ERRDPEWEREEQRRREHEREERRRRERERERERGRGRRDENERDPKREQEERQR---REQE 178 ERRREREQERREREHRGGRDVEDENQRDPDWRREQERRREEEQREREWEREHGRRGRE Y-----EKE-----KRKQQKRYEEQQREDEEKYEERMKEEDNKRDP-----QQREYE 195 RRRREQEQRERERRGERDEEDDEN-QRDPDWRREQ-----ERREQERRRREQEQERRERQ ---DIDWSKY-----DNQDDPQTDCQQCQRRCRQQE 93 ACKKGCGVNQRGSPRAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVDEV 120 MALSKVKLRLCLLAFTLFLACLSVGLGDKGESLSSGAGVDHDGCVNRCEELKGKNVDEFA 60 EQRSREDERRRHERQHGGRSRVNQVAIRRTEQEQSNNPYYFQEQRFQSRYRSDEGHWRVL 412 -----DLINPQRGGSGRYEE-----GEEKQSDNPYYFDERSLSTRFRTEEGHISVL 33.7%; Score 1191.5; DB 2; Length 810; milarity 34.3%; Pred. No. 1.6e-66; Conservative 144; Mismatches 218; Indels 183; Gaps 273 352 292 232 65 227 23;

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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S22477; S22478; S18105; S22050
R;MCHenry, L; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
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S22477
vicilin precursor
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A; Residues: 1-452 < MC2>
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A; Accession: S22478
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A; Residues: 1-566 <MCH>
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 IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL
                                                               LRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIR 342
                                                                                                            ER-GEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPP 175
                                                                                                                                   GRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL
                                                                                                                                                                                       KEQQRQQEEEL - - - -
                                                                                                                                                                                                                                                                LCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQEQCEQRCER---
                                        LKGINDYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVS 235
                                                                                                                                                                                                                        EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQRRCREQQRQH 223
                                                                                                                                                                                                                                                                                 ICEEEEEYNR---QRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
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237; Conserv
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                                                                                                                                                                                                                                                                                                                                        106;
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                                                                                                                                                                                                                                                                                                                                                          Score 1142;
Pred. No. 1.
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C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed eml A; Reference number: $06398
A; Accession: $06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar
C:Accession: S06398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MAINTSNLCSLLFLLSTFLLSTTVSLAE-----SEFD-RQEYEECKRQCMQLETSGQMR 53
                                    LEANPNT FVLPHHCDAEK I Y VVT NGRGTVT FVT HENKESYNVVPGVVVR I PAGSTVY LAN
                                                         LEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLIN 353
                                                                                                                                                                                     NKWREEEEEES----
                                                                                                                                                                                                                      EKYEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGDLINPQ 233
                                                                                                                                                                                                                                                                                            EEYNRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDE 173
                                                                                                                                                                                                                                                                                                                                 Q---DKCEDRSETQLKEEQQRDGEDPQRRYQDCRQHCQQEERRLRP-----HCEQSCREQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFNSQDESIFFPGPRQHQQQSSRSTKQQQPLVSILDF 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPAGSTVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVF
RDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL
                                                                                                                                                                                                                                                            YEKQQQQQPDKQFKECQQRCQWQEQRPERKQQCVKECREQYQEDPWKGER---
                                                                                                                                                                                                                                                                                                                                                                     RCVSQCDKRFEEDIDWSKYDNQDDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEE 113
                                                                                                                                                                                                                                                                                                                                                                                                           MVRNKSVFVVLLE--SLFLSFGLLCSAKDFPGRRSEDDPQQRYEDCRKRC-QLETRGQTE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFNNPDESYFMSFSQQRQRGDER---RGNPLASILDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHAVTFFASKDQPLNAVAFGLNAQNNQRIFLAGK-KNLVRQMDSEAKELSFGVPSKLVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGDVFVAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASGEADVEMACPHLSGRHGGRRGGK--RHEEEEDV-----HYEQVKARLSKREAIVVPV 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVV 514
                                                                                                            -----DEGEQQQRNNPYYFHRRSFQERFREEHGNFRVLQRFADKHHLLRGINEFRIAI
                                                                                                                                               RGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTQREKLEEILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPR----HRGGE--RLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTQAERLRGVLGQQR------EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1092; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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17;

XIX.

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alpha-globulin B precursor (clone C72) - upland cotton
N; Alternate names: seed storage protein; vicilin precursor
C; Species: Gossypium hirsutum (upland cotton)
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C; Accession: A30838; S06911
R; Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A; Title: Developmental biochemistry of cottonseed embryogenesis and germinat A; Reference number: A30838
A; Molecule type: mRNA
A; Residues: 1-588 < CHL>
A; Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A; Experimental source: var. Coker 201
R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A. Title: Developmental biochemistry of Cottonseed ombryogenesis and germinat
                                                                                                                                                                                                                                                                                                                                       A;Title: Developmental biochemistry of cottonseed embryogenesis and ge A;Reference number: $06398
A;Reference number: $06398
A;Accession: $06911
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: I-61 <CH2>
C:Comment: This is a seed storage protein.
C;Superfamily: glycinin
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <STG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local
       246
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                                                                                                                                                                                    35
                                                                                                                                                                                                                     76
                                                                                                                                                                                                      DDPOTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQERC 133
     KQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT
                                                                        YEDCRRRCEQQE--PRQQYQCQRRCREQQRQHGRGGDLINPQR-----GGSGRYEEGEE 245
                                                                                                               R--QQEERQRPQCQQRCLKRFEQEQQQ
                                                                                                                                               QRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQRE 193
                                          FQECQQHCHQQEQRPERKQQCVRECRERYQE - -
                                                                                                                                                                                DDPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONGREYEACPRNEQQQLREVDSSVVAFEINKGSIEVPHYNSKATEVVLVTEGNGHVEMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDLGLLGFGLYNGQDNKRIFVAGKTNNV-RQWDRQAKELAFGVESRLVDEVFNNNPQESY 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKYGQAYEVKPEDY-RQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMA 524
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                      30.7%;
                                                                                                                                                                                                                                                                        Score 1083.5; DB 1; Pred. No. 5.5e-60;
                                                                                                                                                                                                                                                       Mismatches
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                                   -NPWRREREEEAEEEETEEGEQ 175
                                                                                                                                                                                                                                                       182;
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                                                                                                         -SQRQ 123
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A; Residues: 1-509 < CHL>
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                                                                                                                                                                                                                  82
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nes 217; Conserv
                                       FG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGGRQSRRRQQGQGMERKASQEQIRALSQEATSPR----EKSGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.9%;
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alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossyplum hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S08059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERM 180
                                                                                                                                                                                                                                                         LLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLI 352
                                                                                                                                             NRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGV
                                                                                                                                                                                                                        ILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTYYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQRRCREQQRQHGRGGDLINPQRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQRRYEECQQECR--QQEERQQPQCQQRCLKRFEQEQQQ---
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                                                                                                            NQDNKEKLITAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTRSEQLDEL
                                                                                                                                                                                                                                                                                                                                             EEAEEEETEEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROLSDINVTVSALQLNQGSIFVPHYNSKATFVVLVNEGNGYVEMVSPHLPRQSSFEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                      ---GSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQE-----NPWRGERE
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                                 -QQREGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1022.5; DB 2;
Pred. No. 2.8e-56;
"" matches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cottonseed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Genet. 27, 239-251, 1989
A; Title: Characterization of embryo globulins
A; Reference number: A43642; MUID: 89374022
A; Accession: A43642
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A:Title: Molecular basis for allelic polymorphism A:Reference number: A53234; MUID:92090707
A:Accession: A53234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: inbred line Va 26 A; Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-573 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                globulin-15, GLBIS - maize
C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Simhes 203;
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SIANQHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAE 378
                                    LYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE 522
                                                                                                    RLRGVLGQ--QREGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLENKRP 462
                                                                                                                                                                                                TFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAE 407
                                                                                                                                                                                                                                       DYRVAVLEANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGA 199
                                                                                                                                                                                                                                                               NYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGT 347
                                                                                                                                                                                                                                                                                                                    GEGSSEDEREREQEKEEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIR 139
                                                                                                                                                                                                                                                                                                                                           GSG--------YEEGEEKOSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                     EEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSSGNENLLLFAFG-----INAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEEL 627
                                                                                                                                                           VTYLANTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSD
                                                                                                                                                                                                                                                                                                                                                                                              EDDNHHHHGGHKSGRCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD-----RS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNSNPQESYFVS-RQRQRAS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNSQDESIFFPGPRQHQQQS 647
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                                                                             RLERLFGRHGQDKGI.IVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRP
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39.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 902; DB 2;
Pred. No. 9.9e-49;
4; Mismatches 180
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C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C:Accession: B533234; S21824
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize G
A:Reference number: A53234; MUID:92090707
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A;Introns: 167/1; 225/3;
C;Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1; A;Experimental source: inbred line W64A6
A;Note: sequence extracted from NCBI backbone (NCBIP:71285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vicilin-like storage protein Glb1-L, N;Alternate names: globulin-1L
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C; Genetics
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A; Residues: 1-582 <BEL>
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                                                                                                                                                                 NKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMAC
                                                                                                                                                                                                                 GVLGQ--QREGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYS
                                                                                                                                                                                                                                                                                      LANTDGRKKLVITKILHTISVPGEFQFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLE
                                                                                                                                                                                                                                                                                                                           LINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLR 410
                                                                                                                                                                                                                                                                                                                                                            VAVLEANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSG----RYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYR 290
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                                                                                                       PHLSGRHG----GRRGGKRHEEEEDVH-----YEQVKARLSKREAIVVPVGHPVV
                                                                                                                                                                                                                                                                                                                                                                                               LVLLEANPNAFVLPTHLDADATLLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFY 350
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AVASRDSNLQIVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSR
                                                                      PHRQSQGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFV
                                                                                                                                              NQHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVC
                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGSSEDEREQEKEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDDNHHHHGGHKSGQCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD----RS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 895; DB 2; pred. No. 2.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryo - maize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 582;
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믕 S

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RESULT 8
$35221
globulin Begl precursor - barley
globulin Begl precursor - barley
C.Species: Hordeum vulgare (barley)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C.Accession: $35221
R.;Heck, G.R.; Chamberlain, A.K.; HO, T.H.D.
..., Genet. 239, 209-218, 1993
..., Genet. 239, 209-218, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Map position: 4
C:Superfamily: glycinin
C:Keywords: glycoprotein
F:174-190/Product: globulin Begl #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: Begl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:M64372; NID:g167003; C;Genetics:
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A; Residues: 1-637 <HEC>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 227; Conserv
   APRKEVEELFNSQDESI-FFPGPRQHQQQSSRSTKQQQ
                                                                                                                                                                                                                                                                                                                              DNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVLG
                                                    AFVVPPGHPVVEISSSQGSSNLQVVCFEINAERNERVWLAGR-NNVIGKLGSPAQELTFG
                                                                                AIVVPVGHPVVFVSS--GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFA 618
                                                                                                                 PHLGRESESEREHGK--GRRREEEEDDQRQQRRRGSESESEEEEEQQRYETVRARVSRGS
                                                                                                                                                                                 NRHGRLYEADARSFHALANQDVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVQIVC
                                                                                                                                                                                                               NKYGQAYEVKPEDYRQLQDMDVSVFTANITQGSMMGPFFNTRSTKVVVVASGEADVEMAC
                                                                                                                                                                                                                                               QRQGQEKTRSVSIVRASEEQLRELRREAAEGGQGHRWPLPPFRGDSRDTFNLLEQRPKIA
                                                                                                                                                                                                                                                                     QQ-----REGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYS
                                                                                                                                                                                                                                                                                                               DGRRKLVIAKILHTISVPGKF-QFL----SVKPLLASLSKRVLRAAFKTSDERLERLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRG----GDLINPQRGGSG
                                                                                                                                                                                                                                                                                                                                                                          EVNPRAFVVPGFTDADGVGYVAQGEGVLTVIENGEKRSYTVKEGDVIVAPAGSIMHLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EERGRG-----HGRHGEGE-----REEERGRGRGRHGEGEREEEEGRGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEE-----KYEERMKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASHDDEDDRRGGHSLQQCVQRCRQER--PR---YSHARCVQEC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REKGFLPGPEESGGHEEREQEEEEREE
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Pred. No. 5.3e-47;
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                                                                                                                                                 -----VHYEQVKARLSKRE
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
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A; Residues: 1-639 <DOY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 872.5; DB 2
30.7%; Pred. No. 7.7e-47;
tive 147; Mismatches 226
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DЪ Qy DЪ Qy Ъ Qy В δõ Вb δÃ g Q В δÃ В Ωy

Ş д δÃ Вb

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A; Cross references: GB.M13759; NID:g169928; PIDN:AAB01374.1; A; Note: the authors translated the codon GGT for residue 352 R; Schuler, M.A.; Schmitt, E.S.; Beachy, R.N. Nucleic Acids Res. 10, 8225-8244, 1982 A; Title: Closely related families of genes code for the alpha A; Reference number: S16337; MUID:83143288
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J. Biol. Chem. 261, 9228-9238, 1986
A:Title: The glycosylated seed storage proteins of Glycine
A; Reference number: A24810; MUID:86250867
A; Accession: B24810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LLFLLSLFLLSTTVSLAESEFDRQ--EYEECKRQCMQLETSGQMRRCVSQCDKRFEEDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPQQQYEQCQ-ERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEER
                         KVVVVASGEADVEMACPHLSGRHGGRRGGKRHEEEED-VHYEQVKARLSKREAIVVPVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLLLPHHADADYLIVILNGTAILTLYNNDDRDSYNLQSGDALRVPAGTTFYVVNPDNDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKEEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGDLINPQRGGSGR 239
                                                                                         SEDKPFNLGSRDPIYSNKLGKLFEITQRN-PQLRDLDVFLSVVDMNEGALFLPHFNSKAI
                                                                                                                                                      SSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRST
                                                                                                                                                                                                                SYDTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQIRELSKHAKSSSRKTI----S
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beta conglycinin alpha chain precursor - soybean
C:Species: Glycine max (soybean)
C;Detce: 19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-19
C:Accession: S20007
R;Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C.
Plant Mol. Biol. 18, 259-274, 1992
A:Title: Synthesis and assembly of soybean beta-conglycinin in vitro.
A;Reference number: S20007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-605 <LEL>
C;Superfamily: 91ycinin
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                                                                            FGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQ
                                                                                                                                                                                                                                                               KYGQAYEVKPEDYRQLQDMDVSVFŢANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP
                                                                                                                                                                                                                                                                                                                                                               -----GQQR--EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSQSESYFVDAQPQQKEEGNKGRK--GPLSSIL 635
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  QQSSRSTKQQQPLVSIL
                                                 IGINAENNQRNFLAGSQDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKK
                                                                                                                                                                                        HLSGRHGG--RRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFA
                                                                                                                                                                                                                                      KLGKFFEITPEKNPQLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELV--
                                                                                                                                                                                                                                                                                                                                    EGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPFNLRSRDPIYSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YWEKENPKHN--KCLQSCNSERDSYRNQA-CHARCNLLKVEKEECEEGEIPRPRPRPQHP 83
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195; Conser
                                                                                                                                           -GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV--NATSNLNFFA
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31.6%; Pred. No. 4.6e-46;
31.43: Mismatches 210;
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A;Molecule type: Protein
A;Rolecules: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4
A;Experimental source: seed
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
C;Keywords: glycoprotein; seed; storage protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-62/Domain: propeptide #status predicted <PRO>
F;36-605/Product: beta-conglycinin alpha chain #status predicted <MAT>
F;61,517/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-conglycinin alpha chain precursor - soybean C:Species: Glycine max (soybean) C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999 C:Accession: $14681; $74124; $06714 R;Sebastiani, F.L.; Farrell, L.B.; Schuler, M.A.; Beachy, R.N. Plant Mol. Biol. 15, 197-201, 1990 A;Title: Complete sequence of a cDNA of alpha subunit of soybean beta-conglycinin. A;Reference number: $14681; MUID:91355860 A;Accession: $14681
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A;Title: Limited proteolysis of beta-conglycinin and glycinin. A;Reference number: $74123; MUID:97054613
A;Accession: $74124
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A; Residues: 1-605 <SEB>
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                                            HLSGRHGG--RRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFA 584
                                                                                                                                                                                                                                                                                   ENLRLITLAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YWEKENPKHN--KCLQSCNSERDSYRNQA-CHARCNLLKVEKEECEEGEIPRPRPRPQHP
                                                                                             KLGKFFETTPEKNPQLRDLDTFLSTVDMNEGALLLPHFNSKAIVILVINEGDANTELV--
                                                                                                                                       KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP
                                                                                                                                                                                        EGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPFNLRSRDPIYSN
                                                                                                                                                                                                                                                                                                                                                                                                                            PNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNN
-GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV--NATSNLNFFA
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convicilin precursor (clone pJC4) - garden pC; Species: Pisum sativum (garden pea)
C; Species: Pisum sativum (garden pea)
C; Date: 30-Jun-1989 #sequence_revision 30-Ju
C; Accession: S00566
R; Bown, D.; Ellis, T.H.N.; Gatehouse, J.A.
Biochem. J. 251, 717-726, 1988
A; Title: The sequence of a gene encoding con A; Reference number: S00566; MUID: 88326208
A; Accession: S00566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Map position: 2
A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1
C:Superfamily: 91ycinin
F:1-28/Domain: signal sequence #status predicted <SIG>F:29-571/Product: convicilin #status experimental <MAT
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A; Residues: 1-571 <BOW>
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                                                GKLEEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLELL---
                                                                     GQAYEVKPE-DYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPH
                                                                                                                  KRTQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPEYSNKF
                                                                                                                                                                                PVNRPGKFEAF -- GLSENKNQYLRGFSKNILEASLNTKYETIEKVLLEEQEKKPQQLRDR
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                                                                                                                                                                                                                                                                     DADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQ
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Pred. No. 2e-4
10; Mismatches
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-DVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENL:::|||||:||||||
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A; Residues: 1-524 <GRI>
A; Cross references: GB:L06038;
C; Superfamily: alvoinin
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JQ1730
62K sucrose-binding protein precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
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C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted
F;30-524/Product: 62K sucrose-binding protein #st
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A;Title: A 62-kD sucrose binding protein is expressed and A;Reference number: JQ1730; MUID:93104680
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R; Grimes, H.D.;
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                                             ENLLMICFEVNARDNKKFTFAGKD-NIVSSLDNVAKELAFNYPSEMVNGVFLLQRFLERK
                                                                          ENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELF----
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Pred. No. 2.6e-42;
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R; Rodrigo II, M.I.
submitted to the EMBL Data Library, February 1997
A; Reference number: Z15693
A; Accession: T06459
A; Status: preliminary; translated from GB/EMBL/DDB.
A; Molecule type: mRNA
A; Residues: 1-483 < ROD>
A; Cross-references: EMBL:Y11207; PIDN:CAA72090.1
A; Experimental source: var. Lincoln
C; Genetics:
A; Note: p54
C; Superfamily: glycinin
RESULT 15

S24756

Vicilin like storage protein precursor - white spruce C; Species: Picea glauca (white spruce) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #t. C; Accession: S24756; S18873

R. Newton, C.H.; Filnn, B.S.; Sutton, B.C.S.

Plant Mol. Biol. 20, 315-322, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF---LQTIST 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RICMERCD-----DYIKKKQERQKHKEH------EEEEEQEQEEDENPYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQREY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                               LAPKKS----LWPF----GGPFKSPFNIFSNNPAFSNKFGSLFEVGPSQEKSGLEGLNLMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQDMDVSVF 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVNLEPFFESAGRKPESVLNTFSSKVLQAALKSSKGELETVLDEQKKGRIFKIEKEDVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVLGQQREGVIISASQEQIRE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDNDFETKIDTKDGRVLILNKFNEKSKLLKNIENYGLAVLETKANAFLSPHHYDSEAILF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGDLINPQRGGSGRYEEGEEKQSDNPYYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 770.5; DB 2
Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  garden
                                                               10-Sep-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 483;
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                                                               10-Sep-1999
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Best Local
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                                                                                                                                                                                                                                                                                        GVLGQQREGVIISASQEQIRELTRDDSESRRWHIRRG---GESSR----GPYNLFNKRPL 463
                                                                                                                                                                                                                                                                                                                                                                                                                               VLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYL
                               HQQQSSRST
                                                                                               AFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPR-KEVEELFNSQDESIFFPGPRQ 642
                                                                                                                                                                                                                                                                     RIFGGHKSGVIIHANEEQIREMMR-----KRGFSAGSMSAPEHPKPFNLRNQKPD
                                                                                                                                                                                                                                                                                                                                      VNNDDHNTLRIASLVRPVSTVRGEYQPFYVAGGRNPQTVYSAFSDDVLEAAFNTNVQQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162;
RSRDEARSS
                                                                 WFDLNTRGNERQFLAGK-NNVLNTLEREIRQLSFNVPRGEEIEEVLQAQKDQVILRGPQR
                                                                                                                                  ACPHL-GQHGW--SSPRERGDQDITYQRVWAKLRTGSVYIVPAGHPITEIASTNSRLQIL
                                                                                                                                                                  ACPHLSGRHGGRRGGKRHEEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLF
                                                                                                                                                                                                    FENENGRETIAGPKNYPFLDALDVSVGLADLNPGSMTAPSLNSKSTSIGIVTNGEGRIEM
                                                                                                                                                                                                                                     YSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM
                                                                                                                                                                                                                                                                                                                                                                        INRDNNERLHIAKFLQTIST-PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLR 410
                                                                                                                                                                                                                                                                                                                                                                                                          TCIEMKPNTVMLPHYIDATWILYVTRGRGYIAYVHQNELVKRKLEEGDVFGVPSGHTFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEYLGRGRGRR-EEEREENPYVFHSDSFRTRASSEAGEIRALPNFGEVSELLEGIRKFRV
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                                 651
 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 765; DB 1; Pred. No. 2.4e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 448
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